

Resource Summary Report

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GISTIC

RRID:SCR_000151

Type: Tool

Proper Citation

GISTIC (RRID:SCR_000151)

Resource Information

URL: <http://www.mmnt.net/db/0/0/ftp-genome.wi.mit.edu/distribution/GISTIC2.0>

Proper Citation: GISTIC (RRID:SCR_000151)

Description: Software to identify genes targeted by somatic copy-number alterations (SCNAs) that drive cancer growth. By separating SCNA profiles into underlying arm-level and focal alterations, they improve the estimation of background rates for each category.

Abbreviations: GISTIC

Synonyms: GISTIC2.0, GISTIC 2.0, GISTIC 2

Resource Type: software resource

Defining Citation: [PMID:21527027](#)

Keywords: somatic copy-number alteration, gene

Related Condition: Cancer

Availability: Free, Available for download, Freely available

Resource Name: GISTIC

Resource ID: SCR_000151

Alternate IDs: OMICS_02296

License URLs: <Ftp://ftp-genome.wi.mit.edu/distribution/GISTICv2/LICENSE.txt>

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260801T190110+0000

Ratings and Alerts

No rating or validation information has been found for GISTIC.

No alerts have been found for GISTIC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 48 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#).

Morrissey RL, et al. (2026) Elucidating cooperative genetic events in DCIS progression in mutant p53-driven breast cancer. *Proceedings of the National Academy of Sciences of the United States of America*, 123(2), e2526544123.

Siegel F, et al. (2026) Sevabertinib, a Reversible HER2 Inhibitor with Activity in Lung Cancer. *Cancer discovery*, 16(1), 81.

Ku AT, et al. (2025) Radiogenomic Profiling of Prostate Tumors prior to External Beam Radiotherapy Converges on a Transcriptomic Signature of TGF- β Activity Driving Tumor Recurrence. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(24), 5211.

Ren W, et al. (2025) Whole-genome sequencing reveals three follicular lymphoma subtypes with distinct cell of origin and patient outcomes. *Cell reports. Medicine*, 6(8), 102278.

Egea-Rodriguez S, et al. (2025) RECQL4 affects MHC class II-mediated signalling and favours an immune-evasive signature that limits response to immune checkpoint inhibitor therapy in patients with malignant melanoma. *Clinical and translational medicine*, 15(1), e70094.

Lee M, et al. (2025) p16 Immunohistochemical Patterns in Triple-Negative Breast Cancer: Clinical and Genomic Similarities of the p16 Diffuse Pattern to pRB Deficiency. *Pathobiology : journal of immunopathology, molecular and cellular biology*, 92(2), 63.

Xu X, et al. (2025) Genomic Analyses Reveal the Evolving Characteristics of Intestinal Metaplasia and Gastric Cancer. *Cancer research*, 85(16), 3123.

Umeda M, et al. (2024) A new genomic framework to categorize pediatric acute myeloid leukemia. *Nature genetics*, 56(2), 281.

Pinton A, et al. (2024) PHF6-altered T-ALL Harbor Epigenetic Repressive Switch at Bivalent Promoters and Respond to 5-Azacitidine and Venetoclax. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(1), 94.

Plitt G, et al. (2024) The Genomic Landscape of Benign and Malignant Thyroid Tumors from Individuals Carrying Germline PTEN Variants Is Distinct from Sporadic Thyroid Cancers. *Cancer research*, 84(21), 3657.

Krull JE, et al. (2024) Follicular lymphoma B cells exhibit heterogeneous transcriptional states with associated somatic alterations and tumor microenvironments. *Cell reports. Medicine*, 5(3), 101443.

Liu H, et al. (2024) Integrative molecular and spatial analysis reveals evolutionary dynamics and tumor-immune interplay of in situ and invasive acral melanoma. *Cancer cell*, 42(6), 1067.

Kazandjian D, et al. (2024) Genomic Profiling to Contextualize the Results of Intervention for Smoldering Multiple Myeloma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(19), 4482.

Chojnacka M, et al. (2024) Impact of Rare Structural Variant Events in Newly Diagnosed Multiple Myeloma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(3), 575.

Sun Y, et al. (2024) Integrated multi-omics profiling to dissect the spatiotemporal evolution of metastatic hepatocellular carcinoma. *Cancer cell*, 42(1), 135.

Modi A, et al. (2023) Integrative Genomic Analyses Identify LncRNA Regulatory Networks across Pediatric Leukemias and Solid Tumors. *Cancer research*, 83(20), 3462.

Xing X, et al. (2023) Integrated omics landscape of hepatocellular carcinoma suggests proteomic subtypes for precision therapy. *Cell reports. Medicine*, 4(12), 101315.

Jin B, et al. (2023) Immune checkpoint inhibitor-related molecular markers predict prognosis in extrahepatic cholangiocarcinoma. *Cancer medicine*, 12(20), 20470.

Striker SS, et al. (2023) Systematic integration of protein-affecting mutations, gene fusions, and copy number alterations into a comprehensive somatic mutational profile. *Cell reports methods*, 3(4), 100442.

Zhang R, et al. (2023) Urinary Tumor DNA MRD Analysis to Identify Responders to Neoadjuvant Immunotherapy in Muscle-invasive Bladder Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 29(20), 4040.